

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 22:16:34 ; Search time 136 Seconds  
(without alignments)  
261.406 Million cell updates/sec

Title: US-10-671-074-172  
Perfect score: 20  
Sequence: 1 gcttggtgggcaacacat 20

Scoring table: Oligo NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 428752

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Issued Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	55.0	16	3 US-08-485-942A-85	Sequence 85, Appl
2	11	55.0	16	3 US-08-488-214A-85	Sequence 85, Appl
3	11	55.0	16	3 US-08-488-208A-85	Sequence 85, Appl
4	11	55.0	16	3 US-08-483-211A-85	Sequence 85, Appl
5	11	55.0	16	3 US-08-488-223A-85	Sequence 85, Appl
6	11	55.0	16	3 US-08-438-431A-85	Sequence 85, Appl
7	11	55.0	16	3 US-08-488-225A-85	Sequence 85, Appl
8	11	55.0	18	3 US-09-255-893-45	Sequence 45, Appl
9	11	55.0	18	3 US-09-255-893-45	Sequence 46, Appl
10	11	55.0	18	3 US-09-344-521-28	Sequence 28, Appl
11	11	55.0	18	3 US-09-422-978-6545	Sequence 6545, Ap
12	11	55.0	19	2 US-08-690-734A-50	Sequence 50, Appl
13	11	55.0	19	3 US-08-742-185-50	Sequence 50, Appl
14	11	55.0	20	2 US-08-531-556-117	Sequence 117, App
15	11	55.0	20	2 US-08-753-979A-19	Sequence 19, Appl
16	11	55.0	20	3 US-09-230-652-72	Sequence 72, Appl
17	11	55.0	20	3 US-09-198-452A-5551	Sequence 5551, Ap
18	10	50.0	16	3 US-09-052-333A-55	Sequence 55, Appl
19	10	50.0	17	2 US-08-234-613-19	Sequence 19, Appl
20	10	50.0	17	2 US-08-484-192-91	Sequence 91, Appl
21	10	50.0	17	2 US-08-237-973-32	Sequence 32, Appl
22	10	50.0	17	3 US-09-333-611-23	Sequence 23, Appl
23	10	50.0	17	3 US-09-474-432B-431	Sequence 431, App
24	10	50.0	17	3 US-09-476-387-430	Sequence 430, App

c	25	10	50.0	18	2	US-08-432-871C-53	Sequence 53, Appl
	26	10	50.0	18	3	US-09-255-893-44	Sequence 44, Appl
	27	10	50.0	18	3	US-09-071-710-23	Sequence 23, Appl
	28	10	50.0	18	3	US-09-525-397-23	Sequence 23, Appl
	29	10	50.0	18	3	US-09-630-706-21	Sequence 21, Appl
c	30	10	50.0	18	3	US-09-270-956-53	Sequence 53, Appl
	31	10	50.0	19	2	US-08-632-575B-17	Sequence 17, Appl
	32	10	50.0	19	3	US-09-199-542B-17	Sequence 17, Appl
c	33	10	50.0	19	3	US-09-422-978-5558	Sequence 5558, Ap
	34	10	50.0	20	3	US-08-832-985-10	Sequence 10, Appl
c	35	10	50.0	20	3	US-09-158-347-4	Sequence 4, Appl
	36	10	50.0	20	3	US-09-425-638A-15	Sequence 15, Appl
	37	10	50.0	20	3	US-09-543-004-15	Sequence 15, Appl
c	38	10	50.0	20	3	US-09-702-251-45	Sequence 45, Appl
	39	10	50.0	20	3	US-09-410-903-70	Sequence 70, Appl
c	40	10	50.0	20	3	US-09-410-903-76	Sequence 76, Appl
c	41	10	50.0	20	3	US-09-410-903-91	Sequence 91, Appl
c	42	10	50.0	20	3	US-09-360-416-129	Sequence 129, App
c	43	10	50.0	20	3	US-08-835-159-10	Sequence 10, Appl
c	44	10	50.0	20	3	US-09-198-452A-2956	Sequence 2956, Ap
c	45	10	50.0	20	3	US-09-980-052-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1  
US-08-485-942A-85  
; Sequence 85, Application US/08485942A  
; Patent No. 6048837  
; GENERAL INFORMATION:  
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,  
; APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJWALA, AND STEPHEN K. BURR  
; TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS  
; TITLE OF INVENTION: AMENDED)  
; NUMBER OF SEQUENCES: 99  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,942A  
; FILING DATE: JUNE 7, 1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/438,431  
; FILING DATE: May 10, 1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/347,563  
; FILING DATE: No. 6048837ember 30, 1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/292,345  
; FILING DATE: August 17, 1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 85:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; DESCRIPTION: Marker AFM218xf10
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-488-214A-85

Query Match          55.0%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGGGCAACACA 19
   |||||
Db 1 TGGGCAACACA 11

RESULT 3
US-08-488-208A-85
; Sequence 85, Application US/08488208A
; Patent No. 6124448
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,208A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,943
; FILING DATE: June 7, 1995
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6124448ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)

```

; DESCRIPTION: Marker AFM218xf10  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Human  
US-08-488-208A-85

Query Match 55.0%; Score 11; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGGCAACACA 19  
|||||  
Db 1 TGGGCAACACA 11

## RESULT 4

US-08-483-211A-85  
; Sequence 85, Application US/08483211A  
; Patent No. 6309853

## GENERAL INFORMATION:

; APPLICANT: THE ROCKEFELLER UNIVERSITY  
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING  
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC  
; TITLE OF INVENTION: USES THEREOF

; NUMBER OF SEQUENCES: 98

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,211A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/485,943

; FILING DATE: June 7, 1995

; APPLICATION NUMBER: 08/438,431

; FILING DATE: May 10, 1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/347,563

; FILING DATE: No. 6309853ember 30, 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 85:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (primer)

; DESCRIPTION: Marker AFM218xf10

; HYPOTHETICAL: NO

; \*

; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Human  
US-08-483-211A-85

Query Match 55.0%; Score 11; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGGCAACACA 19  
|||||  
Db 1 TGGGCAACACA 11

## RESULT 5

US-08-488-223A-85  
; Sequence 85, Application US/08488223A  
; Patent No. 6350730

## GENERAL INFORMATION:

; APPLICANT: THE ROCKEFELLER UNIVERSITY

; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES TH

; NUMBER OF SEQUENCES: 98

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,223A

; FILING DATE: 07-Jun-1995

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/485,943

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 08/347,563

; FILING DATE: No. 6350730ember 30, 1994

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 85:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (primer)

; DESCRIPTION: Marker AFM218xf10

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Human

; SEQUENCE DESCRIPTION: SEQ ID NO: 85:

US-08-488-223A-85

Query Match 55.0%; Score 11; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Jan 10 10:02:46 2006

us-10-671-074-172.oligo.rni

```
QY      9 TGGGCAACACA 19
Db      1 TGGGCAACACA 11

RESULT 6
US-08-438-431A-85
; Sequence 85, Application US/08438431A
; Patent No. 6429290
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MAFFEI,
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,431A
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6429290ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; DESCRIPTION: Marker AFM218xf10
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-438-431A-85

Query Match      55.0%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 TGGGCAACACA 19
Db      1 TGGGCAACACA 11

RESULT 7
US-08-488-225A-85
; Sequence 85, Application US/08488225A
; Patent No. 6471956
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
```

```
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USE:
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,225A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/483,211
FILING DATE: June 7, 1995
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6471956ember 30, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP2J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
DESCRIPTION: Marker AFM218xf10
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
US-08-488-225A-85

Query Match      55.0%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 TGGGCAACACA 19
Db      1 TGGGCAACACA 11

RESULT 8
US-09-255-893-45
; Sequence 45, Application US/09255893A
; Patent No. 6008344
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
```

APPLICANT: Lex M. Cowert  
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2 GROUP IV EXPRESSION  
FILE REFERENCE: RTS-0055  
CURRENT APPLICATION NUMBER: US/09/255,893A  
CURRENT FILING DATE: 1999-02-23  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 45  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-255-893-45

Query Match 55.0%; Score 11; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAA 15  
|||||  
DB 3 TGGTTGGGCAA 13

## RESULT 9

US-09-255-893-46  
Sequence 46, Application US/09255893A  
Patent No. 6008344  
GENERAL INFORMATION:

APPLICANT: C. Frank Bennett  
APPLICANT: Lex M. Cowert  
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2 GROUP IV EXPRESSION  
FILE REFERENCE: RTS-0055  
CURRENT APPLICATION NUMBER: US/09/255,893A  
CURRENT FILING DATE: 1999-02-23  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 46  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-255-893-46

Query Match 55.0%; Score 11; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAA 15  
|||||  
DB 6 TGGTTGGGCAA 16

## RESULT 10

US-09-344-521-28/c  
Sequence 28, Application US/09344521  
Patent No. 6100990  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: Lex M. Cowert  
TITLE OF INVENTION: ANTISENSE MODULATION OF PI3K P85 EXPRESSION  
FILE REFERENCE: RTS-0062  
CURRENT APPLICATION NUMBER: US/09/344,521  
CURRENT FILING DATE: 1999-06-25  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 28  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-344-521-28

Query Match 55.0%; Score 11; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 TGGTTGGGCAA 15  
|||||  
DB 11 TGGTTGGGCAA 1  
RESULT 11  
US-09-422-978-6545  
Sequence 6545, Application US/09422978  
Patent No. 6537751  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marta  
TITLE OF INVENTION: Biallelic markers for use in constructing a high density....  
FILE REFERENCE: GENSET 020CPI  
CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 6545  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..18  
OTHER INFORMATION: upstream amplification primer 99-12224 for SEQ 2611,  
US-09-422-978-6545

Query Match 55.0%; Score 11; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACA 17  
|||||  
DB 4 GTTGGGCAACA 14

## RESULT 12

US-08-690-734A-50/c  
Sequence 50, Application US/08690734A  
Patent No. 5871920  
GENERAL INFORMATION:  
APPLICANT: Page, David C.  
APPLICANT: Reijo, Renee  
TITLE OF INVENTION: DAZ: A GENE ASSOCIATED WITH AZOOSPERMIA  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,734A  
FILING DATE: 31-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/310,429

```

; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH194-07A
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-690-734A-50

Query Match 55.0%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGGCAACACAT 20
DB 15 GGGCAACACAT 5

RESULT 13
US-08-742-185-50/C
; Sequence 50, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/690,734
; FILING DATE: 31-JUL-1996
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-742-185-50

```

```

Query Match 55.0%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGGCAACACAT 20
DB 15 GGGCAACACAT 5

RESULT 14
US-08-531-556-117/c
; Sequence 117, Application US/08531556
; Patent No. 5776882
; GENERAL INFORMATION:
; APPLICANT: Agoulnik, Alexander I
; APPLICANT: Kent First, Marijo
; APPLICANT: Mualllem, Ariege
; TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
; TITLE OF INVENTION: BATTERY
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,556
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.034CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-531-556-117

Query Match 55.0%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGGCAACACAT 20
DB 15 GGGCAACACAT 5

RESULT 15
US-08-753-979A-19/c
; Sequence 19, Application US/08753979A
; Patent No. 5840549
; GENERAL INFORMATION:
; APPLICANT: Kent First, Marijo
; APPLICANT: Mualllem, Ariege
; TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
; TITLE OF INVENTION: BATTERY
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,979A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-753-979A-19

```

```

Query Match      55.0%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 GGGCAACACAT 20
Db      15 GGGCAACACAT 5

```

```

Search completed: January 10, 2006, 00:13:28
Job time : 137 secs

```

Page Blank (upside)



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 22:32:34 ; Search time 778 Seconds  
(without alignments)  
212.580 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttgggtgggcaacacat 20

Scoring table:

OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134589005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1817556

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Published Applications NA Main.\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	7 US-10-671-074-172	Sequence 172, App
2	19	95.0	20	7 US-10-671-074-40	Sequence 40, Appl
3	19	95.0	20	7 US-10-671-074-118	Sequence 118, App
4	16	80.0	20	7 US-10-671-074-41	Sequence 41, Appl
5	16	80.0	20	7 US-10-671-074-119	Sequence 119, App
6	14	70.0	20	7 US-10-688-706-95	Sequence 95, Appl
7	14	70.0	20	7 US-10-688-706-125	Sequence 125, App
8	14	70.0	20	7 US-10-688-706-141	Sequence 141, App
9	14	70.0	20	7 US-10-688-706-170	Sequence 170, App
10	14	70.0	20	7 US-10-688-706-273	Sequence 273, App
11	14	70.0	20	7 US-10-688-706-695	Sequence 695, App
12	14	70.0	20	7 US-10-688-706-727	Sequence 727, App
13	13	65.0	20	7 US-10-688-706-444	Sequence 444, App
14	13	65.0	20	7 US-10-688-706-1058	Sequence 1058, Ap
15	12	60.0	20	7 US-10-688-706-190	Sequence 190, App
16	12	60.0	20	7 US-10-688-706-229	Sequence 229, App
17	11	55.0	12	8 US-10-257-017B-276516	Sequence 276516,
18	11	55.0	12	8 US-10-257-017B-330753	Sequence 330753,
19	11	55.0	13	8 US-10-257-017B-209229	Sequence 209229,
20	11	55.0	13	8 US-10-257-017B-209230	Sequence 209230,
21	11	55.0	16	3 US-09-736-084-85	Sequence 85, Appl
22	11	55.0	16	8 US-10-730-488-85	Sequence 85, Appl
23	11	55.0	17	3 US-09-780-164-530	Sequence 530, App

ALIGNMENTS

RESULT 1  
US-10-671-074-172  
; Sequence 172, Application US/10671074  
; Publication No. US20040097459A1  
; GENERAL INFORMATION:  
; APPLICANT: Dobie, Kenneth W.  
; APPLICANT: Bhanot, Sanjay  
; APPLICANT: Veniant-Ellison, Murielle  
; APPLICANT: Lindberg, Richard A.  
; APPLICANT: Shutter, John R.  
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION  
; FILE REFERENCE: AMGN0001-101  
; CURRENT APPLICATION NUMBER: US/10/671,074  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: US 10/260,203  
; PRIOR FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 172  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-671-074-172

Query Match 100.0%; Score 20; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTTGGTTGGGCAACACAT 20  
|||||  
Db 1 GCTTTGGTTGGGCAACACAT 20

RESULT 2  
US-10-671-074-40  
; Sequence 40, Application US/10671074  
; Publication No. US20040097459A1  
; GENERAL INFORMATION:  
; APPLICANT: Dobie, Kenneth W.  
; APPLICANT: Bhanot, Sanjay  
; APPLICANT: Veniant-Ellison, Murielle  
; APPLICANT: Lindberg, Richard A.  
; APPLICANT: Shutter, John R.  
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION  
; FILE REFERENCE: AMGN0001-101

Sequence 531, App  
Sequence 532, App  
Sequence 533, App  
Sequence 905, App  
Sequence 6545, Ap  
Sequence 28, Appl  
Sequence 184, App  
Sequence 380, App  
Sequence 3, Appl  
Sequence 77, Appl  
Sequence 17, Appl  
Sequence 72, Appl  
Sequence 551, Ap  
Sequence 101, App  
Sequence 305, App  
Sequence 88, Appl  
Sequence 301, App  
Sequence 275412,  
Sequence 275681,  
Sequence 297223,  
Sequence 297227,  
Sequence 298160,

us-10-671-074-172.oligo.rnpbm

Tue Jan 10 10:02:47 2006

```
;
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-671-074-41

Query Match      80.0%; Score 16; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAAC 16
Db 5 GCTTTGGTTGGCAAC 20

RESULT 5
US-10-671-074-119/c
; Sequence 119, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Ellison, Murielle
; APPLICANT: Lindberg, Richard A.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN0001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-671-074-119

Query Match      80.0%; Score 16; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAAC 16
Db 16 GCTTTGGTTGGCAAC 1

RESULT 6
US-10-688-706-95/c
; Sequence 95, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 95
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-95

Query Match      70.0%; Score 14; DB 7; Length 20;
; SEQ ID NO 41
```

```
;
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-671-074-40

Query Match      95.0%; Score 19; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGCAACACAT 20
Db 1 CTTTGGTTGGCAACACAT 19

RESULT 3
US-10-671-074-118/c
; Sequence 118, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Ellison, Murielle
; APPLICANT: Lindberg, Richard A.
; APPLICANT: Shutter, John R.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN0001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-671-074-118

Query Match      95.0%; Score 19; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGCAACACAT 20
Db 20 CTTTGGTTGGCAACACAT 2

RESULT 4
US-10-671-074-41
; Sequence 41, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Ellison, Murielle
; APPLICANT: Lindberg, Richard A.
; APPLICANT: Shutter, John R.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN0001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 41
```

Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACACAT 20  
|||  
Db 18 GTTGGGCAACACAT 5

Db 18 GTTGGCAACACAT 5

## RESULT 7

```

US-10-688-706-125/c
; Sequence 125, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-125

```

Query Match 70.0%; Score 14; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels

Qy 7 GTTGGGCAACACAT 20  
|||  
Db 20 GTTGGGCAACACAT 7

Db 20 GTTGGGCAACAT 7

## RESULT 8

```

US-10-688-706-141/c
; Sequence 141, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GPAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GPAT antisense
US-10-688-706-141

```

Query Match 70.0%; Score 14; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels

Qy 7 GTTGGGCAACACAT 20  
Db 19 GTTGGGCAACACAT 6

Db 19 GTTGGGCAACACAT 6

## RESULT 9

```

US-10-688-706-170/c
; Sequence 170, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GPAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GPAT antisense
US-10-688-706-170

```

Query Match	70.0%	Score 14;	DB 7;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.6e+02;		
Matches 14;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;				

Qy 7 GTTGGGCAACACAT 20  
| | | | | | | | | |  
Db 17 GTTGGGCAACACAT 4

Db 17 GTTGGGCAACACAT 4

## RESULT 10

```

US-10-688-706-273/c
; Sequence 273, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broscat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 273
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-273

```

Query Match	70.0%;	Score 14;	DB 7;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.6e+02;		
Matches 14;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy 7 GTTGGGCAACACAT 20  
|||  
Db 16 GTTGGGCAACACAT 3

Db 16 GTTGGGCAACACAT 3

## RESULT 11

```

US-10-688-706-695/c
; Sequence 695, Application US/10688706
; Publication No. US20040102412A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01933/1
; CURRENT APPLICATION NUMBER: US/10/688.706

```

[illegible]

Db           |||||||  
              20 TGGCAACACAT 9

Search completed: January 10, 2006, 00:26:41  
Job time : 779 secs

ALL INFORMATION CONTAINED  
HEREIN IS UNCLASSIFIED  
DATE 08-28-2013 BY 60322  
UCBAW/STP

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 22:35:54 ; Search time 320 Seconds  
(without alignments)  
45.567 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttggtgggcaacacat 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4637633 seqs, 364532575 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6446046

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Published Applications NA New:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	12	60.0	19	8	US-11-101-244-619761
c 2	12	60.0	19	8	US-11-101-244-619858
c 3	12	60.0	19	8	US-11-101-244-1014343
c 4	12	60.0	19	8	US-11-101-244-1536666
c 5	12	60.0	19	9	US-11-083-784-619761
c 6	12	60.0	19	9	US-11-083-784-619858
c 7	12	60.0	19	9	US-11-083-784-1014343
c 8	12	60.0	19	9	US-11-083-784-1536666
c 9	11	55.0	19	8	US-11-101-244-90162
c 10	11	55.0	19	8	US-11-101-244-204871
c 11	11	55.0	19	8	US-11-101-244-341693
c 12	11	55.0	19	8	US-11-101-244-352435
c 13	11	55.0	19	8	US-11-101-244-580035
c 14	11	55.0	19	8	US-11-101-244-676846
c 15	11	55.0	19	8	US-11-101-244-694038
c 16	11	55.0	19	8	US-11-101-244-744106
c 17	11	55.0	19	8	US-11-101-244-1071283
c 18	11	55.0	19	8	US-11-101-244-1104410
c 19	11	55.0	19	8	US-11-101-244-1104472
c 20	11	55.0	19	8	US-11-101-244-1279593
c 21	11	55.0	19	8	US-11-101-244-1280905
c 22	11	55.0	19	8	US-11-101-244-1286934
c 23	11	55.0	19	8	US-11-101-244-1286940

24	11	55.0	19	8	US-11-101-244-132286	Sequence 132286,
25	11	55.0	19	8	US-11-101-244-134321	Sequence 134321,
26	11	55.0	19	8	US-11-101-244-1345283	Sequence 1345283,
c 27	11	55.0	19	8	US-11-101-244-1460190	Sequence 1460190,
c 28	11	55.0	19	8	US-11-101-244-1467386	Sequence 1467386,
c 29	11	55.0	19	8	US-11-101-244-1576865	Sequence 1576865,
c 30	11	55.0	19	8	US-11-101-244-1576868	Sequence 1576868,
c 31	11	55.0	19	9	US-11-083-784-90162	Sequence 90162, A
c 32	11	55.0	19	9	US-11-083-784-204871	Sequence 204871,
c 33	11	55.0	19	9	US-11-083-784-341693	Sequence 341693,
c 34	11	55.0	19	9	US-11-083-784-352435	Sequence 352435,
c 35	11	55.0	19	9	US-11-083-784-580035	Sequence 580035,
c 36	11	55.0	19	9	US-11-083-784-676846	Sequence 676846,
c 37	11	55.0	19	9	US-11-083-784-694038	Sequence 694038,
c 38	11	55.0	19	9	US-11-083-784-744106	Sequence 744106,
c 39	11	55.0	19	9	US-11-083-784-1071283	Sequence 1071283,
c 40	11	55.0	19	9	US-11-083-784-1104410	Sequence 1104410,
c 41	11	55.0	19	9	US-11-083-784-1104472	Sequence 1104472,
c 42	11	55.0	19	9	US-11-083-784-1279593	Sequence 1279593,
c 43	11	55.0	19	9	US-11-083-784-1280905	Sequence 1280905,
c 44	11	55.0	19	9	US-11-083-784-1286934	Sequence 1286934,
c 45	11	55.0	19	9	US-11-083-784-1286940	Sequence 1286940,

#### ALIGNMENTS

RESULT 1  
US-11-101-244-619761/c  
; Sequence 619761, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 619761  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-619761

Query Match 60.0%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGGC 13

Db 19 CTTTGGTTGGGC 8

#### RESULT 2

US-11-101-244-619858/c  
; Sequence 619858, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William

Tue Jan 10 10:02:47 2006

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1536666
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1536666

```

```

Query Match      60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGG 12
   ||::||::||
Db 3 GCUUUGGUUGGG 14

```

```

RESULT 5
US-11-083-784-619761/c
; Sequence 619761, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 619761
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-619761

```

```

Query Match      60.0%; Score 12; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGGC 13
   |||||
Db 19 CTTTGGTTGGGC 8

```

```

RESULT 6
US-11-083-784-619858/c
; Sequence 619858, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 619858
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-619858

```

```

Query Match      60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGGC 13
   |||||
Db 19 CTTTGGTTGGGC 8

```

```

RESULT 3
US-11-101-244-1014343
; Sequence 1014343, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1014343
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1014343

```

```

Query Match      60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGGCAACACAT 20
   :|||
Db 6 UGGGCAACACAU 17

```

```

RESULT 4
US-11-101-244-1536666
; Sequence 1536666, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

```



```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 619858
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-619858

```

```

Query Match      60.0%; Score 12; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 CTTTGGTTGGGC 13
Db      19 CTTTGGTTGGGC 8

```

```

RESULT 7
US-11-083-784-1014343
; Sequence 1014343, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1014343
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1014343

```

```

Query Match      60.0%; Score 12; DB 9; Length 19;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      9 TGGCAACACAT 20
Db      6 UGGCAACACAU 17

```

```

RESULT 8
US-11-083-784-1536666
; Sequence 1536666, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1536666
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1536666

```

```

Query Match      60.0%; Score 12; DB 9; Length 19;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GCTTTGGTTGGG 12
Db      3 GCUUUGUUGGG 14

```

```

RESULT 9
US-11-101-244-90162/c
; Sequence 90162, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 90162
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-90162

```

```

Query Match      55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 TTGGTTGGGCA 14
Db      16 TTGGTTGGGCA 6

```

```

RESULT 10
US-11-101-244-204871
; Sequence 204871, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

```

; APPLICANT: Reynolds, Angela									
; APPLICANT: Leake, Devin									
; APPLICANT: Marshall, William									
; APPLICANT: Scaringe, Stephen									
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA									
; FILE REFERENCE: 13499US									
; CURRENT APPLICATION NUMBER: US/11/101,244									
; PRIOR FILING DATE: 2005-04-07									
; PRIOR APPLICATION NUMBER: 60/502,050									
; PRIOR FILING DATE: 2003-09-10									
; PRIOR APPLICATION NUMBER: 60/426,137									
; PRIOR FILING DATE: 2002-11-14									
; NUMBER OF SEQ ID NOS: 1591911									
; SOFTWARE: Proprietary									
; SEQ ID NO 352435									
; LENGTH: 19									
; TYPE: RNA									
; ORGANISM: Homo sapiens									
US-11-101-244-352435									
Query Match 55.0%; Score 11; DB 8; Length 19;									
Best Local Similarity 90.9%; Pred. No. 8.2e+02;									
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
Qy	9	TGGGCAACACA	19						
		:							
Db	6	UGGGCAACACA	16						
RESULT 13									
US-11-101-244-580035/c									
; Sequence 580035, Application US/11101244									
; Publication No. US20050246794A1									
; GENERAL INFORMATION:									
; APPLICANT: Dharmacon, Inc.									
; APPLICANT: Khvorova, Anastasia									
; APPLICANT: Reynolds, Angela									
; APPLICANT: Leake, Devin									
; APPLICANT: Marshall, William									
; APPLICANT: Scaringe, Stephen									
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA									
; FILE REFERENCE: 13499US									
; CURRENT APPLICATION NUMBER: US/11/101,244									
; CURRENT FILING DATE: 2005-04-07									
; PRIOR APPLICATION NUMBER: 60/502,050									
; PRIOR FILING DATE: 2003-09-10									
; PRIOR APPLICATION NUMBER: 60/426,137									
; PRIOR FILING DATE: 2002-11-14									
; NUMBER OF SEQ ID NOS: 1591911									
; SOFTWARE: Proprietary									
; SEQ ID NO 580035									
; LENGTH: 19									
; TYPE: RNA									
; ORGANISM: Homo sapiens									
US-11-101-244-580035									
Query Match 55.0%; Score 11; DB 8; Length 19;									
Best Local Similarity 100.0%; Pred. No. 8.2e+02;									
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	2	CTTTGGTTGGG	12						
Db	18	CTTTGGTTGGG	8						
RESULT 14									
US-11-101-244-676846/c									
; Sequence 676846, Application US/11101244									
; Publication No. US20050246794A1									
; GENERAL INFORMATION:									
; APPLICANT: Dharmacon, Inc.									
; APPLICANT: Khvorova, Anastasia									
; APPLICANT: Reynolds, Angela									

; APPLICANT: Khvorova, Anastasia									
; APPLICANT: Reynolds, Angela									
; APPLICANT: Leake, Devin									
; APPLICANT: Marshall, William									
; APPLICANT: Scaringe, Stephen									
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA									
; FILE REFERENCE: 13499US									
; CURRENT APPLICATION NUMBER: US/11/101,244									
; PRIOR FILING DATE: 2005-04-07									
; PRIOR APPLICATION NUMBER: 60/502,050									
; PRIOR FILING DATE: 2003-09-10									
; PRIOR APPLICATION NUMBER: 60/426,137									
; PRIOR FILING DATE: 2002-11-14									
; NUMBER OF SEQ ID NOS: 1591911									
; SOFTWARE: Proprietary									
; SEQ ID NO 204871									
; LENGTH: 19									
; TYPE: RNA									
; ORGANISM: Homo sapiens									
US-11-101-244-204871									
Query Match 55.0%; Score 11; DB 8; Length 19;									
Best Local Similarity 90.9%; Pred. No. 8.2e+02;									
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
Qy	9	TGGGCAACACA	19						
		:							
Db	8	UGGGCAACACA	18						
RESULT 11									
US-11-101-244-341693/c									
; Sequence 341693, Application US/11101244									
; Publication No. US20050246794A1									
; GENERAL INFORMATION:									
; APPLICANT: Dharmacon, Inc.									
; APPLICANT: Khvorova, Anastasia									
; APPLICANT: Reynolds, Angela									
; APPLICANT: Leake, Devin									
; APPLICANT: Marshall, William									
; APPLICANT: Scaringe, Stephen									
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA									
; FILE REFERENCE: 13499US									
; CURRENT APPLICATION NUMBER: US/11/101,244									
; CURRENT FILING DATE: 2005-04-07									
; PRIOR APPLICATION NUMBER: 60/502,050									
; PRIOR FILING DATE: 2003-09-10									
; PRIOR APPLICATION NUMBER: 60/426,137									
; PRIOR FILING DATE: 2002-11-14									
; NUMBER OF SEQ ID NOS: 1591911									
; SOFTWARE: Proprietary									
; SEQ ID NO 341693									
; LENGTH: 19									
; TYPE: RNA									
; ORGANISM: Homo sapiens									
US-11-101-244-341693									
Query Match 55.0%; Score 11; DB 8; Length 19;									
Best Local Similarity 100.0%; Pred. No. 8.2e+02;									
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	2	CTTTGGTTGGG	12						
Db	18	CTTTGGTTGGG	8						
RESULT 12									
US-11-101-244-352435									
; Sequence 352435, Application US/11101244									
; Publication No. US20050246794A1									
; GENERAL INFORMATION:									
; APPLICANT: Dharmacon, Inc.									
; APPLICANT: Khvorova, Anastasia									
; APPLICANT: Reynolds, Angela									
; APPLICANT: Leake, Devin									
; APPLICANT: Marshall, William									
; APPLICANT: Scaringe, Stephen									
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA									
; FILE REFERENCE: 13499US									
; CURRENT APPLICATION NUMBER: US/11/101,244									
; PRIOR FILING DATE: 2005-04-07									
; PRIOR APPLICATION NUMBER: 60/502,050									
; PRIOR FILING DATE: 2003-09-10									
; PRIOR APPLICATION NUMBER: 60/426,137									
; PRIOR FILING DATE: 2002-11-14									
; NUMBER OF SEQ ID NOS: 1591911									
; SOFTWARE: Proprietary									
; SEQ ID NO 341693									
; LENGTH: 19									
; TYPE: RNA									
; ORGANISM: Homo sapiens									
US-11-101-244-352435									
Query Match 55.0%; Score 11; DB 8; Length 19;									
Best Local Similarity 100.0%; Pred. No. 8.2e+02;									
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	2	CTTTGGTTGGG	12						
Db	18	CTTTGGTTGGG	8						
RESULT 13									
US-11-101-244-580035/c									
; Sequence 580035, Application US/11101244									
; Publication No. US20050246794A1									
; GENERAL INFORMATION:									
; APPLICANT: Dharmacon, Inc.									
; APPLICANT: Khvorova, Anastasia									
; APPLICANT: Reynolds, Angela									
; APPLICANT: Leake, Devin									
; APPLICANT: Marshall, William									
; APPLICANT: Scaringe, Stephen									
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA									
; FILE REFERENCE: 13499US									
; CURRENT APPLICATION NUMBER: US/11/101,244									
; CURRENT FILING DATE: 2005-04-07									
; PRIOR APPLICATION NUMBER: 60/502,050									
; PRIOR FILING DATE: 2003-09-10									
; PRIOR APPLICATION NUMBER: 60/426,137									
; PRIOR FILING DATE: 2002-11-14									
; NUMBER OF SEQ ID NOS: 1591911									
; SOFTWARE: Proprietary									
; SEQ ID NO 580035									
; LENGTH: 19									
; TYPE: RNA									
; ORGANISM: Homo sapiens									
US-11-101-244-580035									
Query Match 55.0%; Score 11; DB 8; Length 19;									
Best Local Similarity 100.0%; Pred. No. 8.2e+02;									
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	2	CTTTGGTTGGG	12						
Db	18	CTTTGGTTGGG	8						
RESULT 14									
US-11-101-244-676846/c									
; Sequence 676846, Application US/11101244									
; Publication No. US20050246794A1									
; GENERAL INFORMATION:									
; APPLICANT: Dharmacon, Inc.									
; APPLICANT: Khvorova, Anastasia									
; APPLICANT: Reynolds, Angela									

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 676846
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-676846
```

```
Query Match      55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      8 TTGGGCAACAC 18
      |||||
Db      17 TTGGGCAACAC 7
```

```
RESULT 15
US-11-101-244-694038
; Sequence 694038, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 694038
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-694038
```

```
Query Match      55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 54.5%; Pred. No. 8.2e+02;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GCTTTGGTTGG 11
      ||::||::||
Db      8 GCUUUGGUUG 18
```

```
Search completed: January 10, 2006, 00:32:13
Job time : 321 secs
```

Handwritten text, possibly a signature or name, oriented vertically.

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 14:18:14 ; Search time 3642 Seconds  
(without alignments)  
256.931 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20  
Sequence: 1 gcttgggtgggaacacat 20

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12980

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database :

EST:\*

1:	gb_est1:*
2:	gb_est2:*
3:	gb_est3:*
4:	gb_hic:*
5:	gb_est4:*
6:	gb_est5:*
7:	gb_est6:*
8:	gb_est7:*
9:	gb_gse1:*
10:	gb_gse2:*
11:	gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	9	45.0	19	9	AZ779085 2M0015B01
C 2	9	45.0	20	9	AZ448577 1M0246A22
C 3	8	40.0	13	6	CF543283 S014680-0
4	8	40.0	14	8	DN987001 MSU_28F_2
5	8	40.0	14	8	DN987019 MSU_28F_2
6	8	40.0	14	8	DN987173 MSU_2F_2
7	8	40.0	14	8	DN988472 ZEBRA_28F
C 8	8	40.0	15	6	CA797315 Cac BL_44
9	8	40.0	15	8	DN987063 MSU_28F_2
10	8	40.0	16	1	AA936037 nz53f05.8
11	8	40.0	16	8	DN987076 MSU_2R_2
12	8	40.0	17	1	AW245605 2827690.3
13	8	40.0	17	8	DN986605 MSU_2F_2
14	8	40.0	18	8	DN986848 MSU_28R_2
15	8	40.0	19	1	AW246512 2821749.3
C 16	8	40.0	19	9	AZ344069 1M0077G21
17	8	40.0	19	9	AZ771432 1M0573003
18	8	40.0	19	9	AZ804081 2M0064118
19	8	40.0	20	1	AJ723010 AJ723010
20	8	40.0	20	3	BM395053 50072-2-7
21	8	40.0	20	7	CO408232 VRK436 Vi
C 22	8	40.0	20	9	AZ369118 1M0119106

C 23	8	40.0	20	9	AZ785716	AZ785716 2M0039F19
C 24	8	40.0	20	9	AZ789409	AZ789409 2M0037H11
C 25	7	35.0	11	5	BQ585171	BQ585171 S014222-0
C 26	7	35.0	12	10	AJ587358	AJ587358 Arabidops
C 27	7	35.0	13	1	AI016863	AI016863 ou27c10.x
C 28	7	35.0	13	5	BQ582420	BQ582420 E012207-0
C 29	7	35.0	15	10	AJ596116	AJ596116 Arabidops
C 30	7	35.0	15	10	AJ600925	AJ600925 Arabidops
C 31	7	35.0	16	1	AI154875	AI154875 ud80f04.r
C 32	7	35.0	16	8	DN988583	DN988583 ZEBRA_28R
C 33	7	35.0	17	1	AJ658902	AJ658902 AJ658902
C 34	7	35.0	17	5	BQ589968	BQ589968 S013719-0
C 35	7	35.0	17	5	BQ789989	BQ789989 hage005AB
C 36	7	35.0	18	5	BQ584776	BQ584776 E011673-0
C 37	7	35.0	18	10	AJ600524	AJ600524 Arabidops
C 38	7	35.0	19	1	AA977115	AA977115 oq24c08.s
C 39	7	35.0	19	1	AI281100	AI281100 qk57h11.x
C 40	7	35.0	19	1	AI688430	AI688430 wc89e09.x
C 41	7	35.0	19	1	AJ663023	AJ663023 AJ663023
C 42	7	35.0	19	6	CA794263	CA794263 Cac BL_12
C 43	7	35.0	19	8	CV998328	CV998328 lv46f09.b
C 44	7	35.0	19	9	AZ334192	AZ334192 1M0063A06
C 45	7	35.0	19	9	AZ339847	AZ339847 1M0071C06

#### ALIGNMENTS

RESULT 1  
AZ779085/c

LOCUS  
AZ779085 19 bp DNA linear GSS 16-FEB-2001

DEFINITION  
2M0015B01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0015B01 F, genomic survey sequence.

ACCESSION  
AZ779085

VERSION  
AZ779085.1 GI:12909385

KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE  
Dunn, D., Aoyagi, A., Barber, M., Bescorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

AUTHORS  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE  
Unpublished (2000)

JOURNAL  
Contact: Robert B. Weiss

COMMENT  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0015 row: B column: 01  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0015B01"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWB42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 45.0%; Score 9; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTGGTTGG 11  
|||||  
Db 14 TTTGGTTGG 6

## RESULT 2

AZ448577/c  
LOCUS 20 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0246A22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0246A22 F, genomic survey sequence.

ACCESSION AZ448577

VERSION AZ448577.1 GI:10601509

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0246 Row: A Column: 22

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

## FEATURES

## source

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0246A22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 45.0%; Score 9; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTGGTTGG 11  
|||||  
Db 20 TTTGGTTGG 12

## RESULT 3

CF543283

LOCUS 13 bp mRNA linear EST 22-SEP-2003

DEFINITION S014680-024-030-D02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone 024-030-D02 5-PRIME, mRNA sequence.

ACCESSION CF543283

VERSION CF543283.1 GI:34891723

KEYWORDS EST.

SOURCE Beta vulgaris

## ORGANISM

Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 13)

Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowek, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

12472698

COMMENT

Contact: Weishaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: [weishaar@mpiz-koeln.mpg.de](mailto:weishaar@mpiz-koeln.mpg.de)

Insert Length: 13 Std Error: 0.00

Plate: 30 Row: D Column: 02

Seq primer: SP6.

## FEATURES

## source

1..13  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:936477"  
/db\_xref="taxon:161934"  
/clone="024-030-D02"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site\_1: SalI; Site\_2: NotI;

cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

## ORIGIN

Query Match 40.0%; Score 8; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CAACACAT 20

Db 1 CAACACAT 8  
|||||

## RESULT 4

DN987001

## LOCUS

DN987001 14 bp mRNA linear EST 17-MAY-2005  
MSU\_28F\_2-II\_04\_MSU\_28F\_2-II\_04\_A04.ab1 Bermudagrass cv. MSU  
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone

## ACCESSION

DN987001

## VERSION

DN987001

## KEYWORDS

EST.

## SOURCE

Cynodon dactylon (Bermuda grass)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Chloridoideae; Cynodonteae; Cynodon.

## REFERENCE

1 (bases 1 to 14)

Melmaiee, K., Elavarthi, S. and Guenzi, A.C.

Identification of differentially expressed genes associated with

cold acclimation using suppression subtraction hybridization (SSH)

and cDNA microarrays

Unpublished (2005)

Contact: Guenzi AC

Dep. of Plant and Soil Sciences

Oklahoma State University

368 Agriculture Hall, Stillwater, OK 74078-6028, USA

Tel: 405-744-6028

Fax: 405-744-6039

Email: [acg@mail.pss.okstate.edu](mailto:acg@mail.pss.okstate.edu)

PCR Primers

FORWARD: M13 Forward

BACKWARD: M13 Reverse

Seq primer: M13 Forward.

Location/Qualifiers

1..14

/organism="Cynodon dactylon"

/mol\_type="mRNA"

/cultivar="MSU"

/db\_xref="taxon:28909"

/clone="MSU\_28F\_2-II\_04\_MSU\_28F\_2-II\_04\_A04.ab1"

/tissue\_type="crown"

/lab\_host="E. coli"

/clone\_lib="Bermudagrass cv. MSU subtracted cold

acclimated cDNA library"

/note="Vector: Qiagen's pDrive; Messenger RNA was

extracted from control and cold acclimated bermudagrass

crown tissue at 2 and 28 days after acclimation and cDNA

library was constructed following Clontech PCR- select

cDNA subtraction procedure."

## ORIGIN

Query Match 40.0%; Score 8; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGT 8

|||||

Db 6 GCTTTGGT 13

## RESULT 5

DN987019

## LOCUS

DN987019 14 bp mRNA linear EST 17-MAY-2005  
MSU\_28F\_2-II\_03\_MSU\_28F\_2-II\_03\_G03.ab1 Bermudagrass cv. MSU  
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone

## DEFINITION

MSU\_28F\_2-II\_03\_MSU\_28F\_2-II\_03\_G03.ab1, mRNA sequence.

## ACCESSION

DN987019

## VERSION

DN987019.1

## KEYWORDS

EST.

## SOURCE

Cynodon dactylon (Bermuda grass)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Chloridoideae; Cynodonteae; Cynodon.

## REFERENCE

1 (bases 1 to 14)

Melmaiee, K., Elavarthi, S. and Guenzi, A.C.

Identification of differentially expressed genes associated with

cold acclimation using suppression subtraction hybridization (SSH)

and cDNA microarrays

Unpublished (2005)

Contact: Guenzi AC

Dep. of Plant and Soil Sciences

Oklahoma State University

368 Agriculture Hall, Stillwater, OK 74078-6028, USA

Tel: 405-744-6028

Fax: 405-744-6039

Email: [acg@mail.pss.okstate.edu](mailto:acg@mail.pss.okstate.edu)

PCR Primers

FORWARD: M13 Forward

BACKWARD: M13 Reverse

Seq primer: M13 Forward.

Location/Qualifiers

1..14

/organism="Cynodon dactylon"

/mol\_type="mRNA"

/cultivar="MSU"

/db\_xref="taxon:28909"

/clone="MSU\_28F\_2-II\_03\_MSU\_28F\_2-II\_03\_G03.ab1"

/tissue\_type="crown"

/lab\_host="E. coli"

/clone\_lib="Bermudagrass cv. MSU subtracted cold

acclimated cDNA library"

/note="Vector: Qiagen's pDrive; Messenger RNA was

extracted from control and cold acclimated bermudagrass

crown tissue at 2 and 28 days after acclimation and cDNA

library was constructed following Clontech PCR- select

cDNA subtraction procedure."

## ORIGIN

Query Match 40.0%; Score 8; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGT 8

|||||

Db 6 GCTTTGGT 13

## RESULT 6

DN987173

## LOCUS

DN987173 14 bp mRNA linear EST 17-MAY-2005  
MSU\_2F\_2-II\_05\_MSU\_2F\_2-II\_05\_G08.ab1 Bermudagrass cv. MSU  
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone

## DEFINITION

MSU\_2F\_2-II\_05\_MSU\_2F\_2-II\_05\_G08.ab1, mRNA sequence.

## ACCESSION

DN987173

## VERSION

DN987173.1

## KEYWORDS

EST.

## SOURCE

Cynodon dactylon (Bermuda grass)

```

ORGANISM      Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
REFERENCE
AUTHORS      1 (bases 1 to 14)
TITLE        Melmaiee,K., Elavarthi,S. and Guenzi,A.C.
IDENTIFICATION of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
JOURNAL      Unpublished (2005)
COMMENT      Contact: Guenzi AC
              Dep. of Plant and Soil Sciences
              Oklahoma State University
              368 Agriculture Hall, Stillwater, OK 74078-6028, USA
              Tel: 405-744-6028
              Fax: 405-744-6039
              Email: acg@mail.pss.okstate.edu
              PCR Primers
              FORWARD: M13 Forward
              BACKWARD: M13 Reverse
              Seq primer: M13 Forward.

FEATURES
source
1..14
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="MSU"
/db_xref="taxon:28909"
/clone="MSU_2F_2-II_05_MSU_2F_2-II_05_G08.abi"
/tissue_type="crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU substracted cold
acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

ORIGIN
Query Match      40.0%; Score 8; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTTGGT 8
        |||||||
Db      6 GCTTTGGT 13

RESULT 7
CA7988472
LOCUS      ZEBRA_28F_2-II_08_ZEBRA_28F_2-II_08_F01.abl 14 bp mRNA linear EST 17-MAY-2005
DEFINITION substracted cold acclimated cDNA library Cynodon dactylon cDNA clone
ZEBRA_28F_2-II_08_ZEBRA_28F_2-II_08_F01.abl, mRNA sequence.
ACCESSION  DN988472
VERSION     DN988472.1 GI:6248299
KEYWORDS    EST.
SOURCE      Cynodon dactylon (Bermuda grass)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
REFERENCE
AUTHORS      1 (bases 1 to 14)
TITLE        Melmaiee,K., Elavarthi,S. and Guenzi,A.C.
IDENTIFICATION of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
JOURNAL      Unpublished (2005)
COMMENT      Contact: Guenzi AC
              Dep. of Plant and Soil Sciences
              Oklahoma State University
              368 Agriculture Hall, Stillwater, OK 74078-6028, USA
              Tel: 405-744-6028

```

```

Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.

FEATURES
source
1..14
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="Zebra"
/db_xref="taxon:28909"
/clone="ZEBRA_28F_2-II_08_ZEBRA_28F_2-II_08_F01.abl"
/tissue_type="crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass line Zebra substracted cold
acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

ORIGIN
Query Match      40.0%; Score 8; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTTGGT 8
        |||||||
Db      6 GCTTTGGT 13

RESULT 8
CA797315/c
LOCUS      Cac BL 4406 Cac BL (Bean and Leaf from Amelonardo type Cacao)
DEFINITION Theobroma cacao cDNA clone Cac_BL_4406 5', mRNA sequence.
ACCESSION  CA797315
VERSION     CA797315.1 GI:26054401
KEYWORDS    EST.
SOURCE      Theobroma cacao (cacao)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
REFERENCE
AUTHORS      Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
              Retzel,E.R. and Jones,C.A.
TITLE        Gene discovery and microarray analysis of cacao (Theobroma cacao
              L.) varieties
JOURNAL      Planta 216 (2), 255-264 (2002)
PUBMED      12447539
COMMENT      Contact: Jones, Paul
              Masterfoods
              3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
              Tel: +44 1664 416644
              Email: Paul.Jones@eu.effem.com
              Seq primer: T3.

FEATURES
source
1..15
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 4406"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
              Cacao)"

```



```

ORIGIN
/note="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

Query Match      40.0%; Score 8; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGGTTGG 11
    |||||
Db 11 TTGGTTGG 4

RESULT 9
DN987063
LOCUS
DEFINITION
MSU 28F 2-II_02_MSU_28F_2-II_02_B02.ab1 mRNA linear EST 17-MAY-2005
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
MSU_28F_2-II_02_MSU_28F_2-II_02_B02.ab1, mRNA sequence.
DN987063
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Cynodon dactylon (Bermuda grass)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
1 (bases 1 to 15)
Melmaisee, K., Elavarthi, S. and Guenzi, A.C.
Identification of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
Unpublished (2005)
Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.

FEATURES
source
1..15
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="MSU"
/db_xref="taxon:28909"
/clone="MSU 28F 2-II_02_MSU_28F_2-II_02_B02.ab1"
/tissue_type="crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU subtracted cold
acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

ORIGIN
Query Match      40.0%; Score 8; DB 8; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGT 8
    |||||
Db 7 GCTTTGGT 14

RESULT 10
AA936037

```

```

LOCUS
DEFINITION
AA936037      16 bp      mRNA      linear      EST 28-APR-1998
n253f05.s1 NCI CGAP Pr12 Homo sapiens cDNA clone IMAGE:1291521
similar to TR:Q28150 Q28150 UNKNOWN PROTEIN ;, mRNA sequence.
AA936037
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuquai, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1291521"
/sex="male"
/tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr12"
/note="Vector: pAMP10; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
NIH."

ORIGIN
Query Match      40.0%; Score 8; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGGGCA 14
    |||||
Db 3 GTTGGGCA 10

RESULT 11
DN987076
LOCUS
DEFINITION
MSU 2R 2-II_02_MSU_2R_2-II_02_H04.abi mRNA linear EST 17-MAY-2005
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
MSU 2R 2-II_02_MSU_2R_2-II_02_H04.abi, mRNA sequence.
DN987076
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Cynodon dactylon (Bermuda grass)
Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
1 (bases 1 to 16)
Melmaisee, K., Elavarthi, S. and Guenzi, A.C.
Identification of differentially expressed genes associated with

```

JOURNAL COMMENT

cold acclimation using suppression subtraction hybridization (SSH) and cDNA microarrays  
Unpublished (2005)  
Contact: Guenzi AC  
Dep. of Plant and Soil Sciences  
Oklahoma State University  
368 Agriculture Hall, Stillwater, OK 74078-6028, USA  
Tel: 405-744-6028  
Fax: 405 744 6039  
Email: acg@mail.pss.okstate.edu

PCR Primers  
FORWARD: M13 Forward  
BACKWARD: M13 Reverse  
Seq primer: M13 Forward.

FEATURES source

1. .16  
/organism="Cynodon dactylon"  
/mol\_type="mRNA"  
/cultivar="MSU"  
/db\_xref="taxon:28909"  
/clone="MSU 2R 2-II\_02\_MSU\_2R\_2-II\_02\_H04.abi"  
/tissue\_type="crown"  
/lab\_host="E. coli"  
/clone\_lib="Bermudagrass cv. MSU subtracted cold acclimated cDNA library"  
/note="Vector: Qiagen's pDrive; Messenger RNA was extracted from control and cold acclimated bermudagrass crown tissue at 2 and 28 days after acclimation and cDNA library was constructed following Clontech PCR- select cDNA subtraction procedure."

ORIGIN

Query Match 40.0%; Score 8; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGT 8  
|||||  
Db 8 GCTTTGGT 15

RESULT 12  
AW245605  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AW245605 17 bp mRNA linear EST 07-JAN-2000  
2822690.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822690 3', mRNA sequence.  
AW245605  
AW245605.1 GI:6588598  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2822690.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center. PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very

JOURNAL COMMENT

Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LICM10 row: B column: 3  
High quality sequence stop: 15.  
Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2822690"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 40.0%; Score 8; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTGGTTG 10  
|||||  
Db 8 TTTGGTTG 15

RESULT 13  
DN986605  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

DN986605 17 bp mRNA linear EST 17-MAY-2005  
MSU 2F 2-II\_03\_MSU\_2F 2-II\_03\_E12.ab1 Bermudagrass cv. MSU subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone  
MSU 2F 2-II\_03\_MSU\_2F 2-II\_03\_E12.ab1, mRNA sequence.  
DN986605  
DN986605.1 GI:66246432  
EST.  
Cynodon dactylon (Bermuda grass)  
Cynodon dactylon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Chloridoideae; Cynodonteae; Cynodon.  
1 (bases 1 to 17)  
Melmaise, K., Blavarthi, S. and Guenzi, A.C.  
Identification of differentially expressed genes associated with cold acclimation using suppression subtraction hybridization (SSH) and cDNA microarrays  
Unpublished (2005)  
Contact: Guenzi AC  
Dep. of Plant and Soil Sciences  
Oklahoma State University  
368 Agriculture Hall, Stillwater, OK 74078-6028, USA  
Tel: 405-744-6028  
Fax: 405 744 6039  
Email: acg@mail.pss.okstate.edu  
PCR Primers  
FORWARD: M13 Forward  
BACKWARD: M13 Reverse  
Seq primer: M13 Forward.

FEATURES source

1. .17  
/organism="Cynodon dactylon"  
/mol\_type="mRNA"  
/cultivar="MSU"  
/db\_xref="taxon:28909"

```

/clone="MSU_2F_2-II_03_MSU_2F_2-II_03_E12.ab1"
/tissue_type="Crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU subextracted cold
acclimated cDNA library"
/notes="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

ORIGIN
Query Match          40.0%; Score 8; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGT 8
Db 9 GCTTTGGT 16
|||||

RESULT 14
DN986848
LOCUS
DEFINITION
MSU_28R_2-II_06_MSU_28R_2-II_06_H11.ab1 mRNA linear EST 17-MAY-2005
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone

ACCESSION
DN986848
VERSION
MSU_28R_2-II_06_MSU_28R_2-II_06_H11.ab1 mRNA sequence.
KEYWORDS
EST.
SOURCE
Cynodon dactylon (Bermuda grass)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
1 (bases 1 to 18)
Melmaise, K., Elavarthi, S. and Guenzi, A.C.
Identification of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
Unpublished (2005)
JOURNAL
COMMENT
Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.

FEATURES
Location/Qualifiers
source
1..18
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="MSU"
/db_xref="taxon:28909"
/clone="MSU_28R_2-II_06_MSU_28R_2-II_06_H11.ab1"
/tissue_type="crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU subextracted cold
acclimated cDNA library"
/notes="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

ORIGIN
Query Match          40.0%; Score 8; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GCTTTGGT 8
Db 10 GCTTTGGT 17
|||||

RESULT 15
AW246512
LOCUS
DEFINITION
AW246512 19 bp mRNA linear EST 07-JAN-2000
2821749.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821749 3',
mRNA sequence.
ACCESSION
AW246512
VERSION
AW246512.1 GI:6589505
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 19)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821749 5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 17
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 19 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: L10M7 row: J column: 22
High quality sequence stop: 17.
Location/Qualifiers
source
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821749"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

## ORIGIN

```

Query Match          40.0%; Score 8; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 TTTGGTTG 10
Db 8 TTTGGTTG 15
|||||

```

us-10-671-074-172.oligo.rst

Tue Jan 10 10:02:47 2006

Search completed: January 10, 2006, 00:09:27  
Job time : 3648 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 08:29:09 ; Search time 2157 Seconds  
(without alignments)  
527.060 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20  
Sequence: 1 gcttggttggaacacacat 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 5881141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 911080

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vi:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	55.0	16	6	ARI175685 Sequence
2	11	55.0	16	6	ARI195261 Sequence
3	11	55.0	16	6	AR222343 Sequence
4	11	55.0	16	6	AR241462 Sequence
5	11	55.0	16	6	BD014828 Modulator
6	11	55.0	17	6	AX217789 Sequence
7	11	55.0	17	6	AX217790 Sequence
8	11	55.0	17	6	AX217791 Sequence
9	11	55.0	17	6	AX217792 Sequence
10	11	55.0	17	6	AX218164 Sequence
11	11	55.0	18	6	AR096847 Sequence
12	11	55.0	18	6	BD088913 Sequence
13	11	55.0	18	6	BD088913 A method
14	11	55.0	18	6	AR294810 Sequence
15	11	55.0	18	11	AB068208 Synthetic
16	11	55.0	19	6	AR035618 Sequence
17	11	55.0	20	6	AR016229 Sequence
18	11	55.0	20	6	AR060253 Sequence

c	19	11	55.0	20	6	BD195406	BD195406 Male infe
c	20	11	55.0	20	6	AR300270	AR300270 Sequence
c	21	11	55.0	20	6	AR315014	AR315014 Sequence
c	22	11	55.0	20	6	AX590861	AX590861 Sequence
c	23	10	50.0	16	6	CS114095	CS114095 Sequence
c	24	10	50.0	17	6	AR009323	AR009323 Sequence
c	25	10	50.0	17	6	AR060788	AR060788 Sequence
c	26	10	50.0	17	6	BD203167	BD203167 Method an
c	27	10	50.0	17	6	I31567	I31567 Sequence 19
c	28	10	50.0	17	6	ARI194070	ARI194070 Sequence
c	29	10	50.0	17	6	AR286059	AR286059 Sequence
c	30	10	50.0	17	6	AR398049	AR398049 Sequence
c	31	10	50.0	17	6	AX217788	AX217788 Sequence
c	32	10	50.0	17	6	AX723794	AX723794 Sequence
c	33	10	50.0	18	6	AR096846	AR096846 Sequence
c	34	10	50.0	18	6	ARI12302	ARI12302 Sequence
c	35	10	50.0	18	6	BD234639	BD234639 Thymidine
c	36	10	50.0	18	6	CQ807628	CQ807628 Sequence
c	37	10	50.0	18	6	CQ827865	CQ827865 Sequence
c	38	10	50.0	18	6	CS038714	CS038714 Sequence
c	39	10	50.0	18	6	E26536	E26536 DTDST gene
c	40	10	50.0	18	6	AR230235	AR230235 Sequence
c	41	10	50.0	18	6	AX046415	AX046415 Sequence
c	42	10	50.0	18	6	AX148881	AX148881 Sequence
c	43	10	50.0	18	6	AX599288	AX599288 Sequence
c	44	10	50.0	18	6	AX796154	AX796154 Sequence
c	45	10	50.0	18	6	AX823114	AX823114 Sequence

ALIGNMENTS

RESULT 1	ARI175685	Sequence 85 from patent US 6309853.	16 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	ARI175685	Sequence 85 from patent US 6309853.	16 bp	DNA	linear	PAT 17-DEC-2001
DEFINITION	Sequence 85 from patent US 6309853.					
ACCESSION	ARI175685					
VERSION	ARI175685.1	GI:17916984				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 16)					
AUTHORS	Friedman, J.M., Zhang, Y. and Proenca, R.					
TITLE	Modulators of body weight, corresponding nucleic acids and proteins, and diagnostic and therapeutic uses thereof					
JOURNAL	Patent: US 6309853-A 85 30-OCT-2001;					
FEATURES	Location/Qualifiers					
source	1..16					
origin	/organism="unknown"					
mol_type	/mol_type="unassigned DNA"					
Query Match	55.0%;	Score 11;	DB 6;	Length 16;		
Best Local Similarity	100.0%;	Pred. No. 1.2e+05;	Mismatches 0;	Indels 0;	Gaps 0;	
Matches	11;	Conservative 0;				
Qy	9	TGGGCAACACA 19				
Db	1	TGGGCAACACA 11				
RESULT 2	ARI195261	Sequence 85 from patent US 6350730.	16 bp	DNA	linear	PAT 20-APR-2002
LOCUS	ARI195261	Sequence 85 from patent US 6350730.	16 bp	DNA	linear	PAT 20-APR-2002
DEFINITION	Sequence 85 from patent US 6350730.					
ACCESSION	ARI195261					
VERSION	ARI195261.1	GI:20244698				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 16)					

AUTHORS Friedman,J.M., Zhang,Y. and Proenca,R. OB polypeptides and modified forms as modulators of body weight JOURNAL Patent: US 6350730-A 85 26-FEB-2002; FEATURES Location/Qualifiers 1. .16 source /organism="unknown" /mol_type="unassigned DNA"		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11	
ORIGIN Query Match Best Local Similarity 55.0%; Score 11; DB 6; Length 16; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11	
RESULT 3 LOCUS DEFINITION Sequence 85 from patent US 6429290. ACCESSION AR222343 VERSION AR222343.1 GI:23329828 KEYWORDS Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 16) Friedman,J.M., Zhang,Y. and Proenca,R. OB polypeptides, modified forms and derivatives JOURNAL Patent: US 6429290-A 85 06-AUG-2002; The Rockefeller University; NYC, NY FEATURES Location/Qualifiers 1. .16 source /organism="unknown" /mol_type="genomic DNA"		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11	
ORIGIN Query Match Best Local Similarity 55.0%; Score 11; DB 6; Length 16; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11	
RESULT 4 LOCUS DEFINITION Sequence 85 from patent US 6471956. ACCESSION AR241462 VERSION AR241462.1 GI:27287152 KEYWORDS Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 16) Friedman,J.M., Zhang,Y. and Proenca,R. Ob polypeptides, modified forms and compositions thereto JOURNAL Patent: US 6471956-A 85 29-OCT-2002; The Rockefeller University; New York, NY FEATURES Location/Qualifiers 1. .16 source /organism="unknown" /mol_type="genomic DNA"		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11	
ORIGIN Query Match Best Local Similarity 55.0%; Score 11; DB 6; Length 16; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11	
RESULT 5 LOCUS DEFINITION Modulator of weight, corresponding nucleic acid and protein, and diagnosis and remedy utilization thereof. ACCESSION BD014828 VERSION BD014828.1 GI:22555635 KEYWORDS JP 2001157591-A/69. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 16) Friedman,J.M., Zhang,Y., Proenca,R., Maffei,M., Halaas,J.L., Kajiwara,K. and Burley,S.K. Modulator of weight, corresponding nucleic acid and protein, and diagnosis and remedy utilization thereof JOURNAL Patent: JP 2001157591-A 69 12-JUN-2001; THE ROCKFELLER UNIVERSITY COMMENT OS Homo sapiens (human) PN JP 2001157591-A/69 PD 12-JUN-2001 PF 29-SEP-2000 JP 2000301496 PR 30-NOV-1994 US 08/347563,10-MAY-1995 US 08/438431 PR 07-JUN-1995 US 08/483211 PI JEFFRY M FRIEDMAN,YIYING ZHANG,RICARDO PROENCA,MARGHERITA PI MAFFEI PI JEFFRY L HALAAS,KETAN KAJIWARA,STEPHEN K BURLEY PC C12N15/09,A61K31/711,A61K38/00,A61K39/395,A61K45/00,A61K48/00, PC A61P3/04, PC A61P3/06,A61P3/10,A61P9/12,C07K14/47,C07K16/18,C12N1/19,C12N1/PC C12N5/10, PC C12N5/10,C12P21/02,C12P21/08,C12O1/68//C12N1/19,C12R1/72), PC (C12N1/19,C12R1:85), (C12N1/19,C12R1:19), (C12N1/19,C12R1:07), PC (C12N1/21,C12R1:46S), (C12N1/21,C12R1:38), (C12N5/10,C12R1:91), PC (C12P21/02,C12R1:19), C12N15/00,A61K37/02,C12N5/00,C12N5/00, PC (C12N5/00,C12R1:91) CC Strandedness: Single; CC Topology: Linear; CC Marker AFM218xf10 FH Key Location/Qualifiers FT source 1. .16 FT Location/Qualifiers 1. .16 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11	
ORIGIN Query Match Best Local Similarity 55.0%; Score 11; DB 6; Length 16; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11	
RESULT 6 LOCUS DEFINITION Sequence 3231 from Patent WO0159103. ACCESSION AX217789 VERSION AX217789.1 GI:15527850 KEYWORDS synthetic construct SOURCE		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11	
ORIGIN Query Match Best Local Similarity 100.0%; Pred. No. 1.2e+05; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11		Qy 9 TGGGCAACACA 19       1 TGGGCAACACA 11	

ORGANISM synthetic construct  
other sequences; artificial sequences.  
1  
REFERENCE  
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 3231 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
ORIGIN  
Query Match 55.0%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CTTTGGTTGGG 12  
|||||  
Db 17 CTTTGGTTGGG 7  
RESULT 7  
AX217790/c  
LOCUS AX217790 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 3232 from Patent WO0159103.  
ACCESSION AX217790  
VERSION AX217790.1 GI:15527851  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 3232 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
ORIGIN  
Query Match 55.0%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CTTTGGTTGGG 12  
|||||  
Db 16 CTTTGGTTGGG 6  
RESULT 8  
AX217791/c  
LOCUS AX217791 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 3233 from Patent WO0159103.  
ACCESSION AX217791  
VERSION AX217791.1 GI:15527852  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression  
JOURNAL Patent: WO 0159103-A 3233 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
ORIGIN  
Query Match 55.0%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CTTTGGTTGGG 12  
|||||  
Db 13 CTTTGGTTGGG 3  
RESULT 9  
AX217792/c  
LOCUS AX217792 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 3234 from Patent WO0159103.  
ACCESSION AX217792  
VERSION AX217792.1 GI:15527853  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 3234 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
ORIGIN  
Query Match 55.0%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CTTTGGTTGGG 12  
|||||  
Db 12 CTTTGGTTGGG 2  
RESULT 10  
AX218164/c  
LOCUS AX218164 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 3606 from Patent WO0159103.  
ACCESSION AX218164  
VERSION AX218164.1 GI:15528225  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 3606 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
Location/Qualifiers

```
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTGGTGGG 12
    |||||
Db 15 CTTGGTGGG 5

RESULT 11
AR096847 18 bp DNA linear PAT 08-SEP-2000
LOCUS
DEFINITION Sequence 45 from patent US 6008344.
ACCESSION AR096847
VERSION AR096847.1 GI:10026014
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS Bennett,C.Frank, and Cowseert,L.M.
TITLE Antisense modulation of phospholipase A2 group IV expression
JOURNAL
FEATURES
source
1..18
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAA 15
    |||||
Db 3 TGGTTGGGCAA 13

RESULT 12
AR096848 18 bp DNA linear PAT 08-SEP-2000
LOCUS
DEFINITION Sequence 46 from patent US 6008344.
ACCESSION AR096848
VERSION AR096848.1 GI:10026016
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS Bennett,C.Frank, and Cowseert,L.M.
TITLE Antisense modulation of phospholipase A2 group IV expression
JOURNAL
FEATURES
source
1..18
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAA 15
    |||||
Db 6 TGGTTGGGCAA 16

RESULT 13
BD088913/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION A method of arraying genome clone.
ACCESSION BD088913
VERSION BD088913.1 GI:22634523
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL
GENOTECs
COMMENT
PN JP 2001321190-A/1157
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001069285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
FT
FT source
1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAA 15
    |||||
Db 17 TGGTTGGGCAA 7

RESULT 14
AR294810 18 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 6545 from patent US 6537751.
ACCESSION AR294810
VERSION AR294810.1 GI:31682094
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL
JOURNAL Patent: US 6537751-A 6545 25-MAR-2003;
Genet S.A.;;
PRX;
FEATURES
source
1..18
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACA 17
```



```

Db      |||||
      4 GTTGGGCAACA 14

RESULT 15
AB068208/c
LOCUS   AB068208          18 bp    DNA        linear    SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, forward primer for human STS sts-R45N15R-2
          at lp36.
ACCESSION AB068208
VERSION   AB068208.1   GI:15129012
KEYWORDS .
SOURCE    synthetic construct
          synthetic construct
          other sequences; artificial sequences.
REFERENCE
AUTHORS   1 Chen, Y.Z., Hayashi, Y., Wu, J.G., Takaoka, E., Maekawa, K.,
            Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
            Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
            and Soeda, E.
            2 A BAC-based STS-content map spanning a 35-Mb region of human
              chromosome 1p35-p36
              Genomics 74 (1), 55-70 (2001)
              11374902
REFERENCE 2 (bases 1 to 18)
AUTHORS   Horii, A.
TITLE     Direct Submission
JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
          Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
          Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
          Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES  Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            misc_feature 1..18
            /note="forward primer for human STS sts-R45N15R-2 at lp36
            sts-R45N15R-2 obtained from clones B23604, B190K13,
            B310A20, B359J17, B45N15, B63P6, B190K13, Human BAC
            library RPCI-11"

ORIGIN
Query Match      55.0%; Score 11; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TGGTTGGGCAA 15
      |||||
Db      17 TGGTTGGGCAA 7

```

Search completed: January 9, 2006, 23:08:30  
 Job time : 2162 secs

Handwritten text, possibly a signature or date, oriented vertically.

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 08:21:43 ; Search time 477 Seconds

(without alignments)  
279.442 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttgggtgggcaacacat 20

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2512440

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : N Geneseq 21.\*

1: geneseqn1980s.\*

2: geneseqn1990s.\*

3: geneseqn2000s.\*

4: geneseqn2001as.\*

5: geneseqn2001bs.\*

6: geneseqn2002as.\*

7: geneseqn2002bs.\*

8: geneseqn2003as.\*

9: geneseqn2003bs.\*

10: geneseqn2003cs.\*

11: geneseqn2003ds.\*

12: geneseqn2004as.\*

13: geneseqn2004bs.\*

14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	ADN97882	Adn97882 Monkey fo
2	20	100.0	20	ADN40818	Adn40818 Monkey fo
3	19	95.0	20	ADN97750	Adn97750 Human fox
C 4	19	95.0	20	ADN97828	Adn97828 Human fox
5	19	95.0	20	ADN40686	Adn40686 Human for
C 6	19	95.0	20	ADN40764	Adn40764 Human for
7	16	80.0	20	ADN97751	Adn97751 Human for
C 8	16	80.0	20	ADN97829	Adn97829 Human for
9	16	80.0	20	ADN40687	Adn40687 Human for
C 10	16	80.0	20	ADN40765	Adn40765 Human for
C 11	14	70.0	20	ADP76896	Adp76896 ChimERIC
C 12	14	70.0	20	ADP76326	Adp76326 ChimERIC
C 13	14	70.0	20	ADP76474	Adp76474 ChimERIC
C 14	14	70.0	20	ADP76296	Adp76296 ChimERIC
C 15	14	70.0	20	ADP76342	Adp76342 ChimERIC
C 16	14	70.0	20	ADP76371	Adp76371 ChimERIC
C 17	14	70.0	20	ADP76928	Adp76928 ChimERIC
C 18	13	65.0	20	ADP76645	Adp76645 ChimERIC
C 19	13	65.0	20	ADP77259	Adp77259 ChimERIC

C 20	12	60.0	20	AAQ95695	AaQ95695 Primer A
C 21	12	60.0	20	ADP76430	Adp76430 ChimERIC
C 22	12	60.0	20	ADP76391	Adp76391 ChimERIC
C 23	11	55.0	12	ABH76523	Abh76523 Oligonuc1
C 24	11	55.0	12	ABI30780	Abi30780 Oligonuc1
C 25	11	55.0	13	ABH09253	Abh09253 Oligonuc1
C 26	11	55.0	13	ABH09252	Abh09252 Oligonuc1
C 27	11	55.0	16	AAT16438	Aat16438 Primer #1
C 28	11	55.0	16	AAC62633	Aac62633 Human OB
C 29	11	55.0	16	AAA12355	Aaa12355 Human OB
C 30	11	55.0	16	AAC62713	Aac62713 Human OB
C 31	11	55.0	16	ABX89587	Abx89587 Human ob
C 32	11	55.0	16	ABL61461	AbL61461 Human ob
C 33	11	55.0	16	ABX96447	Abx96447 Human obe
C 34	11	55.0	16	ADT93218	Adt93218 Human ob
C 35	11	55.0	17	ABK03234	Abk03234 Human CD2
C 36	11	55.0	17	ABK03231	Abk03231 Human CD2
C 37	11	55.0	17	ABK03233	Abk03233 Human CD2
C 38	11	55.0	17	ABK03232	Abk03232 Human CD2
C 39	11	55.0	17	ABK03606	Abk03606 Human CD2
C 40	11	55.0	17	ADP09408	Adp09408 Extend pr
C 41	11	55.0	18	AAx81130	Aax81130 Sark Gene
C 42	11	55.0	18	AAZ56095	Aaz56095 Phospholi
C 43	11	55.0	18	AAZ56096	Aaz56096 Phospholi
C 44	11	55.0	18	AAZ72189	Aaz72189 Human bia
C 45	11	55.0	18	AAAS2034	Aaa52034 Antieense

ALIGNMENTS

RESULT 1

ADN97882  
ID ADN97882 standard; DNA; 20 BP.

AC ADN97882;

DT 01-JUL-2004 (first entry)

DE Monkey foxhead box O1A sequence inhibitory oligo #1.

KW ss; cytostatic; antidiabetic; foxhead box O1A inhibitor;

KW foxhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;

KW diabetes; H-ras gene; antisense; gene expression; primer.

OS Synthetic.

PN WO2004031350-A2.

PD 15-APR-2004.

PF 25-SEP-2003; 2003WO-US030352.

PR 26-SEP-2002; 2002US-00260203.

XX (AMGE-) AMGEN INC.

XX (ISIS-) ISIS PHARM INC.

PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;

XX WPI; 2004-330164/30.

XX New compounds, particularly antisense oligonucleotides, targeted to a  
XX nucleic acid molecule encoding forkhead box O1A, useful for treating  
XX cancer, or type 2 diabetes.

PS Example 25; SEQ ID NO 172; 146pp; English.

CC The invention relates to a compound 8-80 nucleobases in length targeted  
CC to a nucleic acid molecule encoding forkhead box O1A, where the compound  
CC is at least 70% complementary to a nucleic acid molecule encoding  
CC forkhead box O1A and modulates expression of forkhead box O1A by at least  
CC 10%. The compound is useful for treating an animal having a disease or

CC condition associated with forkhead box O1A, e.g. a hyperproliferative  
 CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
 CC sequence corresponds to an oligonucleotide targeted to the monkey forkhead  
 CC box O1A genes in order to inhibit gene expression.

SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTTGGTTGGGCAACACAT 20  
 Db 1 GCTTTGGTTGGGCAACACAT 20

RESULT 2  
 ADN40818  
 ID ADN40818 standard; DNA; 20 BP.  
 XX AC  
 XX ADN40818;  
 XX DT 12-AUG-2004 (first entry)  
 XX DE Monkey forkhead box O1A antisense oligonucleotide #1.  
 XX KW Monkey; forkhead box O1A; ss; antisense oligonucleotide;  
 KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
 KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW type 2 diabetes; cytostatic; antidiabetic.

XX OS Primates.  
 XX US2004097459-A1.  
 XX PN 20-MAY-2004.  
 XX PD 25-SEP-2003; 2003US-00671074.  
 XX PF 26-SEP-2002; 2002US-00260203.  
 XX PR (DORI/) DOBIE K W.  
 XX PA (BHANI/) BHANOT S.  
 XX PA (VENI/) VENIANT-ELLISON M.  
 XX PA (LIND/) LINDBERG R A.  
 XX PA (SHUT/) SHUTTER J R.

XX PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
 XX WPI; 2004-389194/36.  
 XX DR New compounds, particularly antisense oligonucleotides, targeted to a  
 XX PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
 XX PT cancer, or type 2 diabetes.

XX PS Example 25; SEQ ID NO 172; 80pp; English.  
 XX The invention relates to a compound targeted to a nucleic acid molecule  
 XX encoding the human forkhead box O1A polypeptide. The compound is an  
 XX antisense oligonucleotide that specifically hybridizes with the nucleic  
 XX acid and inhibits expression of the polypeptide. The antisense  
 XX oligonucleotide comprises at least one modified internucleoside linkage  
 XX i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
 XX preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
 XX nucleobase comprising a 5-methylcytosine. The antisense compounds are  
 XX useful for modulating the expression of the human forkhead box O1A  
 XX polypeptide and in preparation of a composition for treating  
 XX hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
 XX and type 2 diabetes. This sequence represents an antisense  
 XX oligonucleotide targeted to DNA encoding the monkey forkhead O1A  
 XX polypeptide of the invention.

SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTTGGTTGGGCAACACAT 20  
 Db 1 GCTTTGGTTGGGCAACACAT 20

RESULT 3  
 ADN97750  
 ID ADN97750 standard; DNA; 20 BP.  
 XX AC  
 XX ADN97750;  
 XX DT 01-JUL-2004 (first entry)  
 XX DE Human forkhead box O1A sequence inhibitory oligo #23.  
 XX KW ss; cytostatic; antidiabetic; forkhead box O1A inhibitor;  
 KW forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW diabetes; H-ras gene; antisense; gene expression; primer.  
 XX OS Synthetic.

XX Key Location/Qualifiers  
 XX misc\_difference 1..20  
 XX /tag= b  
 XX /note= "sugar phosphate internucleotide linkages in the  
 XX backbone are replaced with a phosphorothioate  
 XX internucleotide linkages"  
 XX modified\_base 1..20  
 XX /tag= c  
 XX /mod\_base= OTHER  
 XX /note= "all C are 5'-methylcytidines"  
 XX modified\_base 1..5  
 XX /tag= a  
 XX /mod\_base= OTHER  
 XX /note= "nucleotides are 2'-methoxyethyl-nucleotides"  
 XX modified\_base 16..20  
 XX /tag= d  
 XX /mod\_base= OTHER  
 XX /note= "nucleotides are 2'-methoxyethyl-nucleotides"

WO2004031350-A2.

XX PD 15-APR-2004.  
 XX PF 25-SEP-2003; 2003WO-US030352.  
 XX PR 26-SEP-2002; 2002US-00260203.  
 XX XX (AMGE-) AMGEN INC.  
 XX PA (ISIS-) ISIS PHARM INC.

XX PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
 XX WPI; 2004-330164/30.  
 XX DR New compounds, particularly antisense oligonucleotides, targeted to a  
 XX PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
 XX PT cancer, or type 2 diabetes.

XX PS Claim 14; SEQ ID NO 40; 146pp; English.  
 XX The invention relates to a compound 8-80 nucleobases in length targeted  
 XX to a nucleic acid molecule encoding forkhead box O1A, where the compound  
 XX is at least 70% complementary to a nucleic acid molecule encoding  
 XX forkhead box O1A and modulates expression of forkhead box O1A by at least  
 XX 10%. The compound is useful for treating an animal having a disease or  
 XX condition associated with forkhead box O1A, e.g. a hyperproliferative  
 XX disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This

CC sequence corresponds to an oligonucleotide targeted to the human foxhead  
 CC box OIA genes in order to inhibit gene expression.  
 XX  
 SQ Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 U; 0 Other;  
 Query Match 95.0%; Score 19; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CTTTGGTGGCAACACAT 20  
 |||||  
 Db 1 CTTTGGTGGCAACACAT 19  
 |||||  
 RESULT 4  
 ADN97828/c  
 ID ADN97828 standard; DNA; 20 BP.  
 XX  
 AC ADN97828;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human foxhead box OIA gene target sequence #21.  
 XX  
 KW ss: cytostatic; antidiabetic; foxhead box OIA inhibitor;  
 KW foxhead box OIA; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW diabetes; H-ras gene; antisense; gene expression; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02004031350-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 25-SEP-2003; 2003WO-US030352.  
 XX  
 PR 26-SEP-2002; 2002US-00260203.  
 XX  
 PA (AMGE-) AMGEN INC.  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
 XX WPI; 2004-330164/30.  
 DR  
 XX  
 PT New compounds, particularly antisense oligonucleotides, targeted to a  
 PT nucleic acid molecule encoding foxhead box OIA, useful for treating  
 PT cancer, or type 2 diabetes.  
 XX  
 PS Example 18; SEQ ID NO 118; 146pp; English.  
 XX  
 CC The invention relates to a compound 8-80 nucleobases in length targeted  
 CC to a nucleic acid molecule encoding foxhead box OIA, where the compound  
 CC is at least 70% complementary to a nucleic acid molecule encoding  
 CC foxhead box OIA and modulates expression of foxhead box OIA by at least  
 CC 10%. The compound is useful for treating an animal having a disease or  
 CC condition associated with foxhead box OIA, e.g. a hyperproliferative  
 CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
 CC sequence corresponds to a targeted sequence from the human foxhead box  
 CC OIA gene.  
 XX  
 SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 95.0%; Score 19; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CTTTGGTGGCAACACAT 20  
 |||||  
 Db 20 CTTTGGTGGCAACACAT 2  
 |||||  
 RESULT 5

ADN40686  
 ID ADN40686 standard; DNA; 20 BP.  
 XX  
 AC ADN40686;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human foxhead box OIA DNA antisense oligonucleotide #23.  
 XX  
 KW Human; foxhead box OIA; ss; antisense oligonucleotide;  
 KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
 KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW type 2 diabetes; cytostatic; antidiabetic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004097459-A1.  
 XX  
 PD 20-MAY-2004.  
 XX  
 PF 25-SEP-2003; 2003US-00671074.  
 XX  
 PR 26-SEP-2002; 2002US-00260203.  
 XX  
 PA (DOBI/) DOBIE K W.  
 PA (BHAN/) BHANOT S.  
 PA (VENI/) VENIANT-ELLISON M.  
 PA (LIND/) LINDBERG R A.  
 PA (SHUT/) SHUTTER J R.  
 XX  
 PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
 XX WPI; 2004-389194/36.  
 DR  
 XX  
 PT New compounds, particularly antisense oligonucleotides, targeted to a  
 PT nucleic acid molecule encoding foxhead box OIA, useful for treating  
 PT cancer, or type 2 diabetes.  
 XX  
 PS Claim 14; SEQ ID NO 40; 80pp; English.  
 XX  
 CC The invention relates to a compound targeted to a nucleic acid molecule  
 CC encoding the human foxhead box OIA polypeptide. The compound is an  
 CC antisense oligonucleotide that specifically hybridizes with the nucleic  
 CC acid and inhibits expression of the polypeptide. The antisense  
 CC oligonucleotide comprises at least one modified internucleoside linkage,  
 CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
 CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
 CC nucleobase comprising a 5-methylcytosine. The antisense compounds are  
 CC useful for modulating the expression of the human foxhead box OIA  
 CC polypeptide and in preparation of a composition for treating  
 CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
 CC and type 2 diabetes. This sequence represents an antisense  
 CC oligonucleotide targeted to DNA encoding the human foxhead OIA  
 CC polypeptide of the invention.  
 XX  
 SQ Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 U; 0 Other;  
 Query Match 95.0%; Score 19; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CTTTGGTGGCAACACAT 20  
 |||||  
 Db 1 CTTTGGTGGCAACACAT 19  
 |||||  
 RESULT 6  
 ADN40764/c  
 ID ADN40764 standard; DNA; 20 BP.  
 XX  
 AC ADN40764;  
 XX  
 DT 12-AUG-2004 (first entry)

us-10-671-074-172.oligo.rng

Tue Jan 10 10:02:46 2006

```
XX DE Human forkhead box O1A DNA antisense oligonucleotide target region #21.
XX FT Human; forkhead box O1A; ss; antisense oligonucleotide;
XX FT phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;
KW KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;
KW KW type 2 diabetes; cytostatic; antidiabetic.
XX OS Homo sapiens.
XX PN US2004097459-A1.
XX PD 20-MAY-2004.
XX PF 25-SEP-2003; 2003US-00671074.
XX PP 26-SEP-2002; 2002US-00260203.
XX PR (DOBI/) DOBIE K W.
PA (BHAW/) BHANOT S.
PA (VENI/) VENIANT-ELLISON M.
PA (LIND/) LINDBERG R A.
PA (SHUT/) SHUTTER J R.
XX PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;
XX WI WIPI; 2004-389194/36.
XX DR New compounds, particularly antisense oligonucleotides, targeted to a
XX FT nucleic acid molecule encoding forkhead box O1A, useful for treating
XX FT cancer, or type 2 diabetes.
XX PS Example 18; SEQ ID NO 118; 80pp; English.
XX CC The invention relates to a compound targeted to a nucleic acid molecule
XX CC encoding the human forkhead box O1A polypeptide. The compound is an
XX CC antisense oligonucleotide that specifically hybridises with the nucleic
XX CC acid and inhibits expression of the polypeptide. The antisense
XX CC oligonucleotide comprises at least one modified internucleoside linkage
XX CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,
XX CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified
XX CC nucleobase comprising a 5-methylcytosine. The antisense compounds are
XX CC useful for modulating the expression of the human forkhead box O1A
XX CC polypeptide and in preparation of a composition for treating
XX CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,
XX CC and type 2 diabetes. This sequence represents a human forkhead O1A DNA
XX CC antisense oligonucleotide target region of the invention.
XX SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 95.0%; Score 19; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTTTGGTTGGGCAACACAT 20
Db 20 CTTTGGTTGGGCAACACAT 2
RESULT 7
ADN97751
ID ADN97751 standard; DNA; 20 BP.
XX AC ADN97751;
XX XX 01-JUL-2004 (first entry)
XX DE Human forkhead box O1A sequence inhibitory oligo #24.
XX ss; cytostatic; antidiabetic; forkhead box O1A inhibitor;
KW KW forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;
KW KW diabetes; H-ras gene; antisense; gene expression; primer.
XX XX
us-10-671-074-172.oligo.rng
OS Synthetic.
XX Key Location/Qualifiers
XX misc_difference 1..20
FT /tag= b
FT /note= "sugar phosphate internucleotide linkages in the
FT backbone are replaced with a phosphorothioate
FT internucleotide linkages"
FT modified_base 1..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "all C are 5'-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "nucleotides are 2'-methoxyethyl-nucleotides"
FT modified_base 16..20
FT /tag= d
FT /mod_base= OTHER
FT /note= "nucleotides are 2'-methoxyethyl-nucleotides"
WO2004031350-A2.
XX 15-APR-2004.
XX 25-SEP-2003; 2003WO-US030352.
XX 26-SEP-2002; 2002US-00260203.
XX (AMGE-) AMGEN INC.
XX (ISIS-) ISIS PHARM INC.
XX PA Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;
XX WI WIPI; 2004-330164/30.
XX DR New compounds, particularly antisense oligonucleotides, targeted to a
XX FT nucleic acid molecule encoding forkhead box O1A, useful for treating
XX FT cancer, or type 2 diabetes.
XX PS Claim 14; SEQ ID NO 41; 146pp; English.
XX CC The invention relates to a compound 8-80 nucleobases in length targeted
XX CC to a nucleic acid molecule encoding forkhead box O1A, where the compound
XX CC is at least 70% complementary to a nucleic acid molecule encoding
XX CC forkhead box O1A and modulates expression of forkhead box O1A by at least
XX CC 10%. The compound is useful for treating an animal having a disease or
XX CC condition associated with forkhead box O1A, e.g. a hyperproliferative
XX CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This
XX CC sequence corresponds to an oligonucleotide targeted to the human forkhead
XX CC box O1A genes in order to inhibit gene expression.
XX SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 80.0%; Score 16; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTTGGTTGGCAAC 16
Db 5 GCTTTGGTTGGCAAC 20
RESULT 8
ADN97829/c
ID ADN97829 standard; DNA; 20 BP.
XX AC ADN97829;
XX XX 01-JUL-2004 (first entry)
XX DE Human forkhead box O1A gene target sequence #22.
XX XX
```

KW ss; cytostatic; antidiabetic; foxhead box O1A inhibitor;  
KW forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
OS diabetes; H-ras gene; antisense; gene expression; primer.  
XX Homo sapiens.  
PN WO2004031350-A2.  
XX  
PD 15-APR-2004.  
XX  
XX 25-SEP-2003; 2003WO-US030352.  
XX  
XX 26-SEP-2002; 2002US-00260203.  
XX  
XX (AMGE-) AMGEN INC.  
PA (ISIS-) ISIS PHARM INC.  
XX  
XX Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
XX  
XX WPI; 2004-330164/30.  
XX  
XX New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
PT cancer, or type 2 diabetes.  
XX  
XX Example 18; SEQ ID NO 119; 146pp; English.  
XX  
XX The invention relates to a compound 8-80 nucleobases in length targeted  
CC to a nucleic acid molecule encoding forkhead box O1A, where the compound  
CC is at least 70% complementary to a nucleic acid molecule encoding  
CC forkhead box O1A and modulates expression of forkhead box O1A by at least  
CC 10%. The compound is useful for treating an animal having a disease or  
CC condition associated with forkhead box O1A, e.g. a hyperproliferative  
CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
CC sequence corresponds to a targeted sequence from the human foxhead box  
CC O1A gene.  
XX  
SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 80.0%; Score 16; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTTTGGTTGGGCAAC 16  
Db 16 GCTTTGGTTGGGCAAC 1  
RESULT 9  
ADN40687  
ID ADN40687 standard; DNA; 20 BP.  
XX  
XX ADN40687;  
XX  
XX DT 12-AUG-2004 (first entry)  
XX  
XX Human forkhead box O1A DNA antisense oligonucleotide #24.  
XX  
XX Human; forkhead box O1A; ss; antisense oligonucleotide;  
KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
KW type 2 diabetes; cytostatic; antidiabetic.  
XX  
XX Homo sapiens.  
XX  
XX US2004097459-A1.  
PN  
XX 20-MAY-2004.  
XX  
XX 25-SEP-2003; 2003US-00671074.  
XX  
XX 26-SEP-2002; 2002US-00260203.  
XX

PA (DOBI/) DOBIE K W.  
PA (BHAN/) BHANOT S.  
PA (VENI/) VENIANT-ELLISON M.  
PA (LIND/) LINDBERG R A.  
PA (SHUT/) SHUTTER J R.  
XX  
XX Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
PI WPI; 2004-389194/36.  
XX  
XX New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
PT cancer, or type 2 diabetes.  
XX  
XX Claim 14; SEQ ID NO 41; 80pp; English.  
XX  
XX The invention relates to a compound targeted to a nucleic acid molecule  
CC encoding the human forkhead box O1A polypeptide. The compound is an  
CC antisense oligonucleotide that specifically hybridizes with the nucleic  
CC acid and inhibits expression of the polypeptide. The antisense  
CC oligonucleotide comprises at least one modified internucleoside linkage,  
CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
CC nucleobase comprising a 5-methylcytosine. The antisense compounds are  
CC useful for modulating the expression of the human forkhead box O1A  
CC polypeptide and in preparation of a composition for treating  
CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
CC and type 2 diabetes. This sequence represents an antisense  
CC oligonucleotide targeted to DNA encoding the human forkhead O1A  
CC polypeptide of the invention.  
XX  
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
Query Match 80.0%; Score 16; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTTTGGTTGGGCAAC 16  
Db 5 GCTTTGGTTGGGCAAC 20  
RESULT 10  
ADN40765/c  
ID ADN40765 standard; DNA; 20 BP.  
XX  
XX ADN40765;  
XX  
XX DT 12-AUG-2004 (first entry)  
XX  
XX Human forkhead box O1A DNA antisense oligonucleotide target region #22.  
XX  
XX Human; forkhead box O1A; ss; antisense oligonucleotide;  
KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
KW type 2 diabetes; cytostatic; antidiabetic.  
XX  
XX Homo sapiens.  
XX  
XX US2004097459-A1.  
PN  
XX 20-MAY-2004.  
XX  
XX 25-SEP-2003; 2003US-00671074.  
XX  
XX 26-SEP-2002; 2002US-00260203.  
XX  
XX (DOBI/) DOBIE K W.  
PA (BHAN/) BHANOT S.  
PA (VENI/) VENIANT-ELLISON M.  
PA (LIND/) LINDBERG R A.  
PA (SHUT/) SHUTTER J R.  
XX

WPI; 2004-348453/32.

New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase (GFAT), for treating diabetes, a cardiovascular or neurologic disorder, ischemia/reperfusion injury.

Claim 4; SEQ ID NO 695; 175pp; English.

The present invention relates to a compound which specifically hybridizes with a nucleic acid molecule encoding GFAT, and inhibits the expression of GFAT. Specifically claimed are antisense oligonucleotides capable of modulating the expression of GFAT, and which comprise any of the 3063 sequences of 20 base pairs, given in the specification. The compound, composition and methods are useful for treating a disease or condition associated with GFAT, such as a disease or condition, e.g. diabetes, cardiovascular or neurological disorder, ischemia/reperfusion injury. They are also useful in research and diagnostics for modulating the expression of GFAT. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these oligonucleotides inhibit human GFAT expression.

Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 12; Length 20;

Matches	14;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	7	GTGTGGGCACACAT	20						
Db	14	GTGTGGGCACACAT	1						
RESULT 12									
ADP76326/C									
ID	ADP76326 standard; DNA; 20 BP.								
XX	ADP76326;								
XX									
DT	12-AUG-2004 (first entry)								
XX	Chimeric phosphorothioate oligonucleotide #125.								
DE	XX								
KW	GPAT; Antidiabetic; Cardiant;								
KW	Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;								
XX	reperfusion; ss.								
XX	XX								
OS	Synthetic.								
XX	XX								
XX	XX								
Key	Location/Qualifiers								
EH	1								

FT	/*tag= a	
FT	/mod_base= other	
FT	/note= "2-methoxyethyl wing"	
FT	modified_base	17..20
FT	/*tag= b	
FT	/mod_base= other	
FT	/note= "2-methoxyethyl wing"	
XX		
PN	WO2004035763-A2.	
XX		
PD	29-APR-2004.	
XX		
PF	02-OCT-2003; 2003WO-US033332.	
XX		
PR	17-OCT-2002; 2002US-0419268P.	
XX		
PA	(PHAA ) PHARMACIA CORP.	
XX		
PI	Broschat KO, Crosby SD;	
XX		
DR	WPI; 2004-348453/32.	
XX		



PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase  
PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,  
PT ischemia/reperfusion injury.  
XX  
XX  
PS Claim 4; SEQ ID NO 125; 175pp; English.  
XX  
CC The present invention relates to a compound which specifically hybridizes  
CC with a nucleic acid molecule encoding GFAT, and inhibits the expression  
CC of GFAT. Specifically claimed are antisense oligonucleotides capable of  
CC modulating the expression of GFAT, and which comprise any of the 3063  
CC sequences of 20 base pairs, given in the specification. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with GFAT, such as a disease or condition, e.g. diabetes, a  
CC cardiovascular or neurological disorder, ischemia/reperfusion injury.  
CC They are also useful in research and diagnostics for modulating the  
CC expression of GFAT. The present sequence represents a chimeric  
CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these  
CC oligonucleotides inhibit human GFAT expression.  
XX  
SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;  
Query Match 70.0%; Score 14; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GTTGGGCAACACAT 20  
Db 20 GTTGGGCAACACAT 7  
RESULT 13  
ADP76474/c  
ID ADP76474 standard; DNA; 20 BP.  
XX  
XX  
AC ADP76474;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Chimeric phosphorothioate oligonucleotide #273.  
XX  
XX GFAT; Antidiabetic; Cardiant;  
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;  
KW reperfusion; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1...4  
FT /tag= a  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
FT modified\_base 17..20  
FT /tag= b  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
XX  
XX WO2004035763-A2.  
XX  
XX PD 29-APR-2004.  
XX  
XX 02-OCT-2003; 2003WO-US033332.  
XX  
XX 17-OCT-2002; 2002US-0419268P.  
XX  
XX (PHAA ) PHARMACIA CORP.  
XX  
XX Broschat KO, Crosby SD;  
XX  
XX WPI; 2004-348453/32.  
XX  
XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase  
PT

PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,  
PT ischemia/reperfusion injury.  
XX  
XX  
PS Claim 4; SEQ ID NO 273; 175pp; English.  
XX  
CC The present invention relates to a compound which specifically hybridizes  
CC with a nucleic acid molecule encoding GFAT, and inhibits the expression  
CC of GFAT. Specifically claimed are antisense oligonucleotides capable of  
CC modulating the expression of GFAT, and which comprise any of the 3063  
CC sequences of 20 base pairs, given in the specification. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with GFAT, such as a disease or condition, e.g. diabetes, a  
CC cardiovascular or neurological disorder, ischemia/reperfusion injury.  
CC They are also useful in research and diagnostics for modulating the  
CC expression of GFAT. The present sequence represents a chimeric  
CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these  
CC oligonucleotides inhibit human GFAT expression.  
XX  
SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 70.0%; Score 14; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GTTGGGCAACACAT 20  
Db 16 GTTGGGCAACACAT 3  
RESULT 14  
ADP76296/c  
ID ADP76296 standard; DNA; 20 BP.  
XX  
XX  
AC ADP76296;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Chimeric phosphorothioate oligonucleotide #95.  
XX  
XX GFAT; Antidiabetic; Cardiant;  
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;  
KW reperfusion; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1...4  
FT /tag= a  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
FT modified\_base 17..20  
FT /tag= b  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
XX  
XX WO2004035763-A2.  
XX  
XX PD 29-APR-2004.  
XX  
XX 02-OCT-2003; 2003WO-US033332.  
XX  
XX 17-OCT-2002; 2002US-0419268P.  
XX  
XX (PHAA ) PHARMACIA CORP.  
XX  
XX Broschat KO, Crosby SD;  
XX  
XX WPI; 2004-348453/32.  
XX  
XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase  
PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,  
PT ischemia/reperfusion injury.  
PT

XX Claim 4; SEQ ID NO 95; 175pp; English.

XX The present invention relates to a compound which specifically hybridizes

CC with a nucleic acid molecule encoding GFAT, and inhibits the expression

CC of GFAT. Specifically claimed are antisense oligonucleotides capable of

CC modulating the expression of GFAT, and which comprise any of the 3063

CC sequences of 20 base pairs, given in the specification. The compound,

CC composition and methods are useful for treating a disease or condition,

CC associated with GFAT, such as a disease or condition, e.g. diabetes, a

CC cardiovascular or neurological disorder, ischemia/reperfusion injury.

CC They are also useful in research and diagnostics for modulating the

CC expression of GFAT. The present sequence represents a chimeric

CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these

CC oligonucleotides inhibit human GFAT expression.

XX

SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACACAT 20

Db 18 GTTGGGCAACACAT 5

Search completed: January 9, 2006, 22:32:18

Job time : 483 secs

XX The present invention relates to a compound which specifically hybridizes

CC with a nucleic acid molecule encoding GFAT, and inhibits the expression

CC of GFAT. Specifically claimed are antisense oligonucleotides capable of

CC modulating the expression of GFAT, and which comprise any of the 3063

CC sequences of 20 base pairs, given in the specification. The compound,

CC composition and methods are useful for treating a disease or condition,

CC associated with GFAT, such as a disease or condition, e.g. diabetes, a

CC cardiovascular or neurological disorder, ischemia/reperfusion injury.

CC They are also useful in research and diagnostics for modulating the

CC expression of GFAT. The present sequence represents a chimeric

CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these

CC oligonucleotides inhibit human GFAT expression.

XX

SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACACAT 20

Db 18 GTTGGGCAACACAT 5

RESULT 15

ADP76342/c

ID ADP76342 standard; DNA; 20 BP.

XX

AC ADP76342;

XX

DT 12-AUG-2004 (first entry)

XX

DE Chimeric phosphorothioate oligonucleotide #141.

XX

GFAT; Antidiabetic; Cardiant;

KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;

KW reperfusion; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 1..4

FT /\*tag= a

FT /mod\_base= other

FT /note= "2-methoxyethyl wing"

FT modified\_base 17..20

FT /\*tag= b

FT /mod\_base= other

FT /note= "2-methoxyethyl wing"

XX

WO2004035763-A2.

PN

XX

29-APR-2004.

PD

XX

02-OCT-2003; 2003WO-US033332.

PF

XX

17-OCT-2002; 2002US-0419268P.

PR

XX

(PHAA ) PHARMACIA CORP.

PA

XX

Broschat KO, Crosby SD;

PI

XX

WPI; 2004-348453/32.

DR

XX

New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase

PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,

PT ischemia/reperfusion injury.

XX

Claim 4; SEQ ID NO 141; 175pp; English.

PS